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Amendments to the Specification:

Please replace the current Sequence Listing with the Sequence Listing attached hereto both as a paper copy (21 pages) and in computer readable form (CRF) on floppy disk.

Please amend the paragraph on page 4, line 33, through page 5, line 13, as set forth below.

Figure 3 depicts the mutations in *PKD2* from an analysis of genomic PCR products in three *PKD2* families. Left panel shows the results of direct sequencing of genomic PCR products from affected individuals. The arrows denote double peaks, confirmed by sequencing in both directions, indicative of heterozygosity at that nucleotide. Each of the mutant alleles results in a premature stop codon. The right panel demonstrates segregation of the mutated allele with the disease phenotype. In families 97 and 1605, the affected alleles are not digested by Bsr I and Taq I, respectively, since the restriction sites are lost by mutation. Family 1601 shows segregation of the single strand conformational analysis (SSCA) variant, indicated by the arrow, with the disease phenotype. For each family, only portions of more extensive pedigrees are shown. Filled symbols, affected individuals. Open symbols, unaffected individuals. M, 100 bp ladder. Family 97 - SEQ ID NO:13, Family 1605 - SEQ ID NO:14, Family 1601 - SEQ ID NO:15.